BUNDESREPUBLIK DEUTSCHLAND

PCT/EP 98 / 0 5 1 2 7

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Bescheinigung

REC   1 0 DEC 1998

Die Firma Memorec Stoffel GmbH in Köln/Deutschland hat eine Patentanmeldung unter der Bezeichnung

"Neutrale Sphingomyelinase der Maus und des Menschen und diese überxprimierende Säuger- und Nicht-Säugerzellen"

als Zusatz zur Patentanmeldung 197 34 764.9

am 15. Oktober 1997 beim Deutschen Patentamt eingereicht.

Das angeheftete Stück ist eine richtige und genaue Wiedergabe der ursprünglichen Unterlage dieser Patentanmeldung.
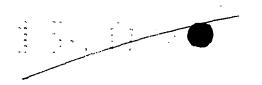
Die Anmeldung hat im Deutschen Patentamt vorläufig die Symbole C 12 N, C 12 Q und G 01 N der Internationalen Patentklassifikation erhalten.

München, den 22. Oktober 1998
Der Präsident des Deutschen Patentamts
Im Auftrag

Agurks

Aktenzeich n: <u>197 58 501.9</u>

murine nSMase

```
   1  GTGCTGGTGG AAGCCGAGCC GGGAACAAGG GAGGAACCTG TAGGMCGCGG
  51  TGCGGAGAAC CCACCGAAGG ACCTAAGAAT CTGGAACAGT CCACCCGAGA
 101  TTCCTTCCAG GACTGCCGGC GGCCTCGCGC AGCCAGCCCG GGATTTGCAG
 151  CCGACCTTCT TTCCGGGTGG AAGGACGGCC TTTGTCCCAG TAACGCAGGA
 201  GTAGCCCCCC ACCCCCAACC AGCTCGCGTT CCTGGGTCGG GGCAGCGCAG
 251  GACAGGGCAA TAAGCCTGTG CGCGCAATCC GCCTCGCCGC CCTTGCTCCG
 301  AAGCACTCCA GCCATGAAGC TCAACTTTTC TCTACGGCTG AGAGTTTTCA
 351  ATCTCAACTG CTGGGACATC CCCTACCTGA GCAAACATAG GGCGGACCGC
 401  ATGAAGCGCT TGGGAGACTT TCTGAACTTG GAAAACTTTG ATCTGGCTCT
 451  CCTGGAGGAG GTGTGGAGTG AGCAGGACTT CCAGTACCTA AGGCAAAGGC
 501  TATCGCTCAC CTATCCAGAT GCACACTACT TCAGAAGCGG GATGATAGGC
 551  AGTGGCCTCT GTGTGTTCTC CAAACACCCA ATCCAGGAAA TCTTCCAGCA
 601  TGTCTACAGT CTGAATGGTT ACCCCTACAT GTTCCATCAT GGAGACTGGT
 651  TCTGTGGGAA GTCTGTGGGG CTGCTGGTGC TCCGTCTAAG TGGACTGGTG
 701  CTCAATGCCT ACGTGACTCA TCTACATGCT GAGTACAGCC GACAGAAGGA
 751  CATCTACTTT GCACACCGTG TGGCCCAAGC TTGGGAACTG GCCCAGTTCA
 801  TCCACCACAC ATCCAAGAAT GCAGATGTGG TTCTATTGTG TGGAGACCTC
 851  AATATGCACC CCAAAGACCT GGGCTGCTGC CTGCTGAAAG AGTGGACAGG
 901  GCTCCATGAT GCTTTCGTTG AGACTGAGGA CTTTAAGGGC TCTGATGATG
 951  GCTGTACCAT GGTACCCAAG AACTGCTACG TCAGCCAGCA GGACCTGGGA
1001  CCGTTTCCGT CTGGTATCCG GATTGATTAC GTGCTTTACA AGGCAGTCTC
1051  TGAGTTCCAC GTCTGCTGTG AGACTCTGAA AACCACTACA GGCTGTGACC
1101  CTCACAGTGA CAAGCCCTTC TCTGATCACG AGGCCCTCAT GGCTACTTTG
1151  TATGTGAAGC ACAGCCCCCC TCAGGAAGAC CCCTGTACTG CCTGTGGCCC
1201  ACTGGAAAGG TCCGATTTGA TCAGCGTGCT AAGGGAGGCc AGGACAGAGC
1251  TGGGGCTAGG CATAGCTAAA GCTCGCTGGT GGGCTGCATT CTCTGGCTAT
1301  GTGATCGTTT GGGGGCTGTC CCTTCTGGTG TTGCTGTGTG TCCTGGCTGC
1351  AGGAGAAGAG GCCAGGGAAG TGGCCATCAT CCTCTGCATA CCCAGTGTGG
1401  GTCTGGTGCT GGTAGCAGGT GCAGTCTACC TCTTCCACAA GCAGGAGGCC
1451  AAGGGCTTAT GTCGGGCCCA GGCTGAGATG CTGCACGTTC TGACAAGGGA
1501  AACGGAGACC CAGGACCGAG GCTCAGAGCC TCACCTAGCC TACTGCTTGC
1551  AGCAGGAGGG GGACAGAGCT TAAGAGCTTA ACAATAAAAC TTGCTTGACA
1601  CACAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA
```

human nSMase

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    1  GACCGCCGGG GACGAGCTTG GAGGAAAAGG AACCGGGAGC CGCCCACCCG
   51  GGGGCGCTCT CCGGACCCCC AGGGTCCTAG CGCGCGGCCC TTACCGAGCC
  101  TGGGCGCCCG GATTTCGGGA GCGGATCGCC TTTCCGGGTT GGCGGCCCGC
  151  CTGATTGGGA ACAGCCGGCC GGTTGCCGGG GGAACGCGGG AGTCGGGCCC
  201  GACCTGAGCC ACGCGGGCTT GGTGCCCACC TGTGCGCGCC GCCTGCGAAG
  251  AAGGAACGGT CTAGGGAGAA GGCGCCGCCG CCGCCCCCG TCCCCACCGC
  301  GGCCGTCGCT GGAGAGTTCG AGCCGCCTAG CGCCCTGGA GCTCCCCAAC
  351  CATGAAGCTC AACTTCTCCC TGCGACTGCG GATCTTCAAC CTCAACTGCT
  401  GGGGCATTCC GTACTTGAGC AAGCACCGGG CCGACCGCAT GAGGCGCCTG
  451  GGAGACTTTC TGAACCAGGA GAGCTTCGAC CTGGCTTTGC TGGAGGAGGT
  501  GTGGAGTGAG CAGGACTTCC AGTACCTGAG ACAGAAGCTG TCACCTACCT
  551  ACCCAGCTGC ACACCACTTC CGGAGCGGAA TCATTGGCAG TGGCCTCTGT
  601  GTCTTCTCCA AACATCCAAT CCAGGAGCTT ACCCAGCACA TCTACACTCT
  651  CAATGGCTAC CCCTACATGA TCCATCATgg tgactggttc agTGGGAAGG
  701  CTGTGGGGCT GCTGGTGCTC CATCTAAGTG GCATGGTGCT CAACGCCTAT
  751  GTGACCCATC TCCATGCCGA ATACAATCGA CAGAAGGACA TCTACCTAGC
  801  ACATCGTGTG GCCCAAGCTT GGGAATTGGC CCAGTTCATC CACCACACAT
  851  CCAAGAAGGC AGACGTGGTT CTGTTGTGTG GAGACCTCAA CATGCACCCA
  901  GAAGACCTGG GCTGCTGCCT GCTGAAGGAG TGGACAGGGC TTCATGATGC
  951  CTATCTTGAA ACTCGGGACT TCAAGGGCTC TGAGGAAGGC AACACAATGG
 1001  TACCCAAGAA CTGCTACGTC AGCCAGCAGG AGCTGAAGCC ATTTCCCTTT
 1051  GGTGTCCGCA TTGACTACGT GCTTTACAAG GCAGTTTCTG GGTTTTACAT
 1101  CTCCTGTAAG AGTTTTGAAA CCACTACAGG CTTTGACCCT CACAGTGGCA
 1151  CCCCCCTCTC TGATCATGAA GCCCTGATGG CTACTCTGTT TGTGAGGCAC
 1201  AGCCCCCCAC AGCAGAACCC CAGCTCTACC CACGGACCAG CAGAGAGGTC
 1251  GCCGTTGATG TGTGTGCTAA AGGAGGCCTG GACGGAGCTG GGTCTGGGCA
 1301  TGGCTCAGGC TCGCTGGTGG GCCACCTTCG CTAGCTATGT GATTGGCCTG
 1351  GGGCTGCTTC TCCTGGCACT GCTGTGTGTC CTGGCGGCTG GAGGAGGGGC
 1401  CGGGGAAGCT GCCATACTGC TCTGGACCCC CAGTGTAGGG CTGGTGCTGT
 1451  GGGCAGGTGC ATTCTACCTC TTCCACGTAC AGGAGGTCAA TGGCTTATAT
 1501  AGGGCCCAGG CTGAGCTCCA GCATGTGCTA GGAAGGGCAA GGGAGGCCCA
 1551  GGATCTGGGC CCAGAGCCTC AGCCAGCCCT ACTCCTGGGG CAGCAGGAGG
 1601  GGGACAGAAC TAAAGAACAA TAAAGCTTGG CCCTTTAAAA AAAAAAAAAA
 1651  AAAA
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mouse nSMase transl. [313 to 1572] -> 1-phase Translation

DNA sequence   1632 b.p.   GTGCTGGTGGAA ... AAAAAAAAAAAA   linear

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313 /   1                          343 /  11
ATG AAG CTC AAC TTT TCT CTA CGG CTG AGA GTT TTC AAT CTC AAC TGC TGG GAC ATC CCC
met lys leu asn phe ser leu arg leu arg val phe asn leu asn cys trp asp ile pro
373 /  21                          403 /  31
TAC CTG AGC AAA CAT AGG GCG GAC CGC ATG AAG CGC TTG GGA GAC TTT CTG AAC TTG GAA
tyr leu ser lys his arg ala asp arg met lys arg leu gly asp phe leu asn leu glu
433 /  41                          463 /  51
AAC TTT GAT CTG GCT CTC CTG GAG GAG GTG TGG AGT GAG CAG GAC TTC CAG TAC CTA AGG
asn phe asp leu ala leu leu glu glu val trp ser glu gln asp phe gln tyr leu arg
493 /  61                          523 /  71
CAA AGG CTA TCG CTC ACC TAT CCA GAT GCA CAC TAC TTC AGA AGC GGG ATG ATA GGC AGT
gln arg leu ser leu thr tyr pro asp ala his tyr phe arg ser gly met ile gly ser
553 /  81                          583 /  91
GGC CTC TGT GTG TTC TCC AAA CAC CCA ATC CAG GAA ATC TTC CAG CAT GTC TAC AGT CTG
gly leu cys val phe ser lys his pro ile gln glu ile phe gln his val tyr ser leu
613 / 101                          643 / 111
AAT GGT TAC CCC TAC ATG TTC CAT CAT GGA GAC TGG TTC TGT GGG AAG TCT GTG GGG CTG
asn gly tyr pro tyr met phe his his gly asp trp phe cys gly lys ser val gly leu
673 / 121                          703 / 131
CTG GTG CTC CGT CTA AGT GGA CTG GTG CTC AAT GCC TAC GTG ACT CAT CTA CAT GCT GAG
leu arg leu ser gly leu val leu asn ala tyr val thr his leu his ala glu
      141                          763 / 151
CGA CAG AAG GAC ATC TAC TTT GCA CAC CGT GTG GCC CAA GCT TGG GAA CTG GCC
tyr ser arg gln lys asp ile tyr phe ala his arg val ala gln ala trp glu leu ala
793 / 161                          823 / 171
CAG TTC ATC CAC CAC ACA TCC AAG AAT GCA GAT GTG GTT CTA TTG TGT GGA GAC CTC AAT
gln phe ile his his thr ser lys asn ala asp val val leu leu cys gly asp leu asn
853 / 181                          883 / 191
ATG CAC CCC AAA GAC CTG GGC TGC TGC CTG CTG AAA GAG TGG ACA GGG CTC CAT GAT GCT
met his pro lys asp leu gly cys cys leu leu lys glu trp thr gly leu his asp ala
913 / 201                          943 / 211
TTC GTT GAG ACT GAG GAC TTT AAG GGC TCT GAT GAT GGC TGT ACC ATG GTA CCC AAG AAC
phe val glu thr glu asp phe lys gly ser asp asp gly cys thr met val pro lys asn
973 / 221                          1003 / 231
TGC TAC GTC AGC CAG CAG GAC CTG GGA CCG TTT CCG TCT GGT ATC CGG ATT GAT TAC GTG
cys tyr val ser gln gln asp leu gly pro phe pro ser gly ile arg ile asp tyr val
1033 / 241                         1063 / 251
CTT TAC AAG GCA GTC TCT GAG TTC CAC GTC TGC TGT GAG ACT CTG AAA ACC ACT ACA GGC
leu tyr lys ala val ser glu phe his val cys cys glu thr leu lys thr thr thr gly
1093 / 261                         1123 / 271
TGT GAC CCT CAC AGT GAC AAG CCC TTC TCT GAT CAC GAG GCC CTC ATG GCT ACT TTG TAT
cys asp pro his ser asp lys pro phe ser asp his glu ala leu met ala thr leu tyr
1153 / 281                         1183 / 291
CAC AGC CCC CCT CAG GAA GAC CCC TGT ACT GCC TGT GGC CCA CTG GAA AGG TCC
his ser pro pro gln glu asp pro cys thr ala cys gly pro leu glu arg ser
1213 / 301                         1243 / 311
GAT TTG ATC AGC GTG CTA AGG GAG GCc AGG ACA GAG CTG GGG CTA GGC ATA GCT AAA GCT
asp leu ile ser val leu arg glu ala arg thr glu leu gly leu gly ile ala lys ala
1273 / 321                         1303 / 331
CGC TGG TGG GCT GCA TTC TCT GGC TAT GTG ATC GTT TGG GGG CTG TCC CTT CTG GTG TTG
arg trp trp ala ala phe ser gly tyr val ile val trp gly leu ser leu leu val leu
1333 / 341                         1363 / 351
CTG TGT GTC CTG GCT GCA GGA GAA GAG GCC AGG GAA GTG GCC ATC ATC CTC TGC ATA CCC
leu cys val leu ala ala gly glu glu ala arg glu val ala ile ile leu cys ile pro
1393 / 361                         1423 / 371
AGT GTG GGT CTG GTG CTG GTA GCA GGT GCA GTC TAC CTC TTC CAC AAG CAG GAG GCC AAG
ser val gly leu val leu val ala gly ala val tyr leu phe his lys gln glu ala lys
1453 / 381                         1483 / 391
GGC TTA TGT CGG GCC CAG GCT GAG ATG CTG CAC GTT CTG ACA AGG GAA ACG GAG ACC CAG
gly leu cys arg ala gln ala glu met leu his val leu thr arg glu thr glu thr gln
1513 / 401                         1543 / 411
GAC CGA GGC TCA GAG CCT CAC CTA GCC TAC TGC TTG CAG CAG GAG GGG GAC AGA GCT TAA
asp arg gly ser glu pro his leu ala tyr cys leu gln gln glu gly asp arg ala OCH
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human nSMase transl. [352 to 1623] -> 1-phase Translation

DNA sequence 1654 b.p. GACCGCCGGGGA ... AAAAAAAAAAAA linear

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352 /   1                         382 /  11
ATG AAG CTC AAC TTC TCC CTG CGA CTG CGG ATC TTC AAC CTC AAC TGC TGG GGC ATT CCG
met lys leu asn phe ser leu arg leu arg ile phe asn leu asn cys trp gly ile pro
412 /  21                         442 /  31
TAC TTG AGC AAG CAC CGG GCC GAC CGC ATG AGG CGC CTG GGA GAC TTT CTG AAC CAG GAG
tyr leu ser lys his arg ala asp arg met arg arg leu gly asp phe leu asn gln glu
472 /  41                         502 /  51
AGC TTC GAC CTG GCT TTG CTG GAG GAG GTG TGG AGT GAG CAG GAC TTC CAG TAC CTG AGA
ser phe asp leu ala leu leu glu glu val trp ser glu gln asp phe gln tyr leu arg
532 /  61                         562 /  71
CAG AAG CTG TCA CCT ACC TAC CCA GCT GCA CAC CAC TTC CGG AGC GGA ATC ATT GGC AGT
gln lys leu ser pro thr tyr pro ala ala his his phe arg ser gly ile ile gly ser
592 /  81                         622 /  91
GGC CTC TGT GTC TTC TCC AAA CAT CCA ATC CAG GAG CTT ACC CAG CAC ATC TAC ACT CTC
gly leu cys val phe ser lys his pro ile gln glu leu thr gln his ile tyr thr leu
652 / 101                         682 / 111
AAT GGC TAC CCC TAC ATG ATC CAT CAt ggt gac tgg ttc agT GGG AAG GCT GTG GGG CTG
asn gly tyr pro tyr met ile his his gly asp trp phe ser gly lys ala val gly leu
712 / 121                         742 / 131
CTG GTG CTC CAT CTA AGT GGC ATG GTG CTC AAC GCC TAT GTG ACC CAT CTC CAT GCC GAA
val leu his leu ser gly met val leu asn ala tyr val thr his leu his ala glu
    141                          802 / 151
  CGA CAG AAG GAC ATC TAC CTA GCA CAT CGT GTG GCC CAA GCT TGG GAA TTG GCC
tyr asn arg gln lys asp ile tyr leu ala his arg val ala gln ala trp glu leu ala
832 / 161                         862 / 171
CAG TTC ATC CAC CAC ACA TCC AAG AAG GCA GAC GTG GTT CTG TTG TGT GGA GAC CTC AAC
gln phe ile his his thr ser lys lys ala asp val val leu leu cys gly asp leu asn
892 / 181                         922 / 191
ATG CAC CCA GAA GAC CTG GGC TGC TGC CTG CTC AAG GAG TGG ACA GGG CTT CAT GAT GCC
met his pro glu asp leu gly cys cys leu leu lys glu trp thr gly leu his asp ala
952 / 201                         982 / 211
TAT CTT GAA ACT CGG GAC TTC AAG GGC TCT GAG GAA CGC AAC ACA ATG GTA CCC AAG AAC
tyr leu glu thr arg asp phe lys gly ser glu glu gly asn thr met val pro lys asn
1012 / 221                        1042 / 231
TGC TAC GTC AGC CAG CAG GAG CTG AAG CCA TTT CCC TTT GGT GTC CGC ATT GAC TAC GTG
cys tyr val ser gln gln glu leu lys pro phe pro phe gly val arg ile asp tyr val
1072 / 241                        1102 / 251
CTT TAC AAG GCA GTT TCT GGG TTT TAC ATC TCC TGT AAG AGT TTT GAA ACC ACT ACA GGC
leu tyr lys ala val ser gly phe tyr ile ser cys lys ser phe glu thr thr thr gly
1132 / 261                        1162 / 271
TTT GAC CCT CAC AGT GGC ACC CCC CTC TCT GAT CAT GAA GCC CTG ATG GCT ACT CTG TTT
phe asp pro his ser gly thr pro leu ser asp his glu ala leu met ala thr leu phe
1192 / 281                        1222 / 291
  G CAC AGC CCC CCA CAG CAG AAC CCC AGC TCT ACC CAC GGA CCA GCA GAG AGG TCG
  his ser pro pro gln gln asn pro ser ser thr his gly pro ala glu arg ser
    301                          1282 / 311
CCG TTG ATG TGT GTG CTA AAG GAG GCC TGG ACG GAG CTG GGT CTG GGC ATG GCT CAG GCT
pro leu met cys val leu lys glu ala trp thr glu leu gly leu gly met ala gln ala
1312 / 321                        1342 / 331
CGC TGG TGG GCC ACC TTC GCT AGC TAT GTG ATT GGC CTG GGG CTG CTT CTC CTG GCA CTG
arg trp trp ala thr phe ala ser tyr val ile gly leu gly leu leu leu leu ala leu
1372 / 341                        1402 / 351
CTG TGT GTC CTG GCG GCT GGA GGA GGG GCC GGG GAA GCT GCC ATA CTG CTC TGG ACC CCC
leu cys val leu ala ala gly gly gly ala gly glu ala ala ile leu leu trp thr pro
1432 / 361                        1462 / 371
AGT GTA GGG CTG GTG CTG TGG GCA GGT GCA TTC TAC CTC TTC CAC GTA CAG GAG GTC AAT
ser val gly leu val leu trp ala gly ala phe tyr leu phe his val gln glu val asn
1492 / 381                        1522 / 391
GGC TTA TAT AGG GCC CAG GCT GAG CTC CAG CAT GTG CTA GGA AGG GCA AGG GAG GCC CAG
gly leu tyr arg ala gln ala glu leu gln his val leu gly arg ala arg glu ala gln
1552 / 401                        1582 / 411
GAT CTG GGC CCA GAG CCT CAG CCA GCC CTA CTC CTG GGG CAG CAG GAG GGG GAC AGA ACT
asp leu gly pro glu pro gln pro ala leu leu leu gly gln gln glu gly asp arg thr
1612 / 421
AAA GAA CAA TAA
lys glu gln OCH
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 801  ACATCGTGTG GCCCAAGCTT GGGAATTGGC CCAGTTCATC CACCACACAT
 851  CCAAGAAGGC AGACGTGGTT CTGTTGTGTG GAGACCTCAA CATGCACCCA
 901  GAAGACCTGG GCTGCTGCCT GCTGAAGGAG TGGACAGGGC TTCATGATGC
 951  CTATCTTGAA ACTCGGGACT TCAAGGGCTC TGAGGAAGGC AACACAATGG
1001  TACCCAAGAA CTGCTACGTC AGCCAGCAGG AGCTGAAGCC ATTTCCCTTT
1051  GGTGTCCGCA TTGACTACGT GCTTTACAAG GCAGTTTCTG GGTTTTACAT
1101  CTCCTGTAAG AGTTTTGAAA CCACTACAGG CTTTGACCCT CACAGTGGCA
1151  CCCCCCTCTC TGATCATGAA GCCCTGATGG CTACTCTGTT TGTGAGGCAC
1201  AGCCCCCCAC AGCAGAACCC CAGCTCTACC CACGGACCAG CAGAGAGGTC
1251  GCCGTTGATG TGTGTGCTAA AGGAGGCCTG GACGGAGCTG GGTCTGGGCA
1301  TGGCTCAGGC TCGCTGGTGG GCCACCTTCG CTAGCTATGT GATTGGCCTG
1351  GGGCTGCTTC TCCTGGCACT GCTGTGTGTC CTGGCGGCTG GAGGAGGGGC
1401  CGGGGAAGCT GCCATACTGC TCTGGACCCC CAGTGTAGGG CTGGTGCTGT
1451  GGGCAGGTGC ATTCTACCTC TTCCACGTAC AGGAGGTCAA TGGCTTATAT
1501  AGGGCCCAGG CTGAGCTCCA GCATGTGCTA GGAAGGGCAA GGGAGGCCCA
1551  GGATCTGGGC CCAGAGCCTC AGCCAGCCCT ACTCCTGGGG CAGCAGGAGG
1601  GGGACAGAAC TAAAGAACAA TAAAGCTTGG CCCTTTAAAA AAAAAAAAAA
1651  AAAA
```

underlined is the coding sequence

mouse nSMase

```
   1  GTGCTGGTGG AAGCCGAGCC GGGAACAAGG GAGGAACCTG TAGGMCGCGG
  51  TGCGGAGAAC CCACCGAAGG ACCTAAGAAT CTGGAACAGT CCACCCGAGA
 101  TTCCTTCCAG GACTGCCGGC GGCCTCGCGC AGCCAGCCCG GGATTTGCAG
 151  CCGACCTTCT TTCCGGGTGG AAGGACGGCC TTTGTCCCAG TAACGCAGGA
 201  GTAGCCCCCC ACCCCCAACC AGCTCGCGTT CCTGGGTCGG GGCAGCGCAG
 251  GACAGGGCAA TAAGCCTGTG CGCGCAATCC GCCTCGCCGC CCTTGCTCCG
 301  AAGCACTCCA GCCATGAAGC TCAACTTTTC TCTACGGCTG AGAGTTTTCA
 351  ATCTCAACTG CTGGGACATC CCCTACCTGA GCAAACATAG GCGGGACCGC
 401  ATGAAGCGCT TGGGAGACTT TCTGAACTTG GAAAACTTTG ATCTGGCTCT
 451  CCTGGAGGAG GTGTGGAGTG AGCAGGACTT CCAGTACCTA AGGCAAAGGC
 501  TATCGCTCAC CTATCCAGAT GCACACTACT TCAGAAGCGG GATGATAGGC
 551  AGTGGCCTCT GTGTGTTCTC CAAACACCCA ATCCAGGAAA TCTTCCAGCA
 601  TGTCTACAGT CTGAATGGTT ACCCCTACAT GTTCCATCAT GGAGACTGGT
 651  TCTGTGGGAA GTCTGTGGGG CTGCTGGTGC TCCGTCTAAG TGGACTGGTG
 701  CTCAATGCCT ACGTGACTCA TCTACATGCT GAGTACAGCC GACAGAAGGA
 751  CATCTACTTT GCACACCGTG TGGCCCAAGC TTGGGAACTG GCCCAGTTCA
 801  TCCACCACAC ATCCAAGAAT GCAGATGTGG TTCTATTGTG TGGAGACCTC
 851  AATATGCACC CCAAAGACCT GGGCTGCTGC CTGCTGAAAG AGTGGACAGG
 901  GCTCCATGAT GCTTTCGTTG AGACTGAGGA CTTTAAGGGC TCTGATGATG
 951  GCTGTACCAT GGTACCCAAG AACTGCTACG TCAGCCAGCA GGACCTGGGA
1001  CCGTTTCCGT CTGGTATCCG GATTGATTAC GTGCTTTACA AGGCAGTCTC
1051  TGAGTTCCAC GTCTGCTGTG AGACTCTGAA AACCACTACA GGCTGTGACC
1101  CTCACAGTGA CAAGCCCTTC TCTGATCACG AGGCCCTCAT GGCTACTTTG
1151  TATGTGAAGC ACAGCCCCCC TCAGGAAGAC CCCTGTACTG CCTGTGGCCC
1201  ACTGGAAAGG TCCGATTTGA TCAGCGTGCT AAGGGAGGCc AGGACAGAGC
1251  TGGGGCTAGG CATAGCTAAA GCTCGCTGGT GGGCTGCATT CTCTGGCTAT
1301  GTGATCGTTT GGGGGCTGTC CCTTCTGGTG TTGCTGTGTG TCCTGGCTGC
1351  AGGAGAAGAG GCCAGGGAAG TGGCCATCAT CCTCTGCATA CCCAGTGTGG
1401  GTCTGGTGCT GGTAGCAGGT GCAGTCTACC TCTTCCACAA GCAGGAGGCC
1451  AAGGGCTTAT GTCGGGCCCA GGCTGAGATG CTGCACGTTC TGACAAGGGA
1501  AACGGAGACC CAGGACCGAG GCTCAGAGCC TCACCTAGCC TACTGCTTGC
1551  AGCAGGAGGG GGACAGAGCT TAAGAGCTTA ACAATAAAAC TTGCTTGACA
1601  CACAAAAAAA AAAAAAAAAA AAAAAAAAA AAA
```

human nSMase

```
   1  GACCGCCGGG GACGAGCTTG GAGGAAAAGG AACCGGGAGC CGCCCACCCG
  51  GGGGCGCTCT CCGGACCCCC AGGGTCCTAG CGCGCGGCCC TTACCGAGCC
 101  TGGGCGCCCG GATTTCGGGA GCGGATCGCC TTTCCGGGTT GGCGGCCCGC
 151  CTGATTGGGA ACAGCCGGCC GGTTGCCGGG GAACGCGGG AGTCGGGCCC
 201  GACCTGAGCC ACGCGGGCTT GGTGCCCACC TGTGCGCGCC GCCTGCGAAG
 251  AAGGAACGGT CTAGGGAGAA GGCGCCGCCG GCCGCCCCCG TCCCCACCGC
 301  GGCCGTCGCT GGAGAGTTCG AGCCGCCTAG CGCCCCTGGA GCTCCCCAAC
 351  CATGAAGCTC AACTTCTCCC TGCGACTGCG GATCTTCAAC CTCAACTGCT
 401  GGGGCATTCC GTACTTGAGC AAGCACCGGG CCGACCGCAT GAGGCGCCTG
 451  GGAGACTTTC TGAACCAGGA GAGCTTCGAC CTGGCTTTGC TGGAGGAGGT
 501  GTGGAGTGAG CAGGACTTCC AGTACCTGAG ACAGAAGCTG TCACCTACCT
 551  ACCCAGCTGC ACACCACTTC CGGAGCGGAA TCATTGGCAG TGGCCTCTGT
 601  GTCTTCTCCA AACATCCAAT CCAGGAGCTT ACCCAGCACA TCTACACTCT
 651  CAATGGCTAC CCCTACATGA TCCATCAtgg tgactggttc agTGGGAAGG
 701  CTGTGGGGCT GCTGGTGCTC CATCTAAGTG GCATGGTGCT CAACGCCTAT
 751  GTGACCCATC TCCATGCCGA ATACAATCGA CAGAAGGACA TCTACCTAGC
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